

0570  
07/17

# 10



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/941,193A

DATE: 07/23/2002 8-6  
TIME: 13:04:51

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\07232002\I941193A.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BROW, MARY ANN D.

7 LYAMICHEV, VICTOR I.

8 OLIVE, DAVID M.

10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

11 PATHOGENS

13 (iii) NUMBER OF SEQUENCES: 165

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MEDLEN & CARROLL

17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200

18 (C) CITY: SAN FRANCISCO

19 (D) STATE: CALIFORNIA

20 (E) COUNTRY: UNITED STATES OF AMERICA

21 (F) ZIP: 94104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/941,193A

C--> 31 (B) FILING DATE: 28-Aug-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: CARROLL, PETER G.

36 (B) REGISTRATION NUMBER: 32,837

37 (C) REFERENCE/DOCKET NUMBER: FORS-01756

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410

41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 2506 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 ATGAGGGGGA TGCTGCCCT CTTTGAGCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC 60

60 CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG 120

62 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC 180

64 GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG 240

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66 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG      300
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72 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCCA CCCCAGAGGG      480
74 TACCTCATCA CCCCGGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA CCAGTGGGCC      540
76 GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG      600
78 GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC      660
80 CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG      720
82 CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTGCGCAAA      780
84 AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC      840
86 CTCCTCCACG AGTTCGGCCT TCTGGAAAGC CCAAGGCCCC TGGAGGAGGC CCCCTGGCCC      900
88 CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCCGAT      960
90 CTTCTGGCCC TGGCCGCCGC CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA     1020
92 GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG CTTCTCGCCA AAGACCTGAG CGTTCTGGCC     1080
94 CTGAGGGAAG GCCTTGGCCT CCCGCCGGGC GACGACCCCA TGCTCCTCGC CTACCTCCTG     1140
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98 GAGGCGGGGG AGCGGGCCGC CTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT     1260
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104 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC      1440
106 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT      1500
108 CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC CGTCTGGAG      1560
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114 CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC      1740
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122 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCTT GATGCGCCGG      1980
124 GCGGCCAAGA CCATCAACTT CGGGGTCTCT TACGGCATGT CGGCCACCGC CCTCTCCAG      2040
126 GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC      2100
128 CCAAGGTGCG GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG      2160
130 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG      2220
132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCCTCC AGGGCACCAG CGCCGACCTC      2280
134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC      2340
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138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCTT GGAGGTGGAG      2460
140 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC      2506
142 (2) INFORMATION FOR SEQ ID NO: 2:
144     (i) SEQUENCE CHARACTERISTICS:
145         (A) LENGTH: 2496 base pairs
146         (B) TYPE: nucleic acid
147         (C) STRANDEDNESS: double
148         (D) TOPOLOGY: linear
150     (ii) MOLECULE TYPE: DNA (genomic)
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
156 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGG CGGCCACCAC      60
158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCTTCACCA CCAGCCGCGG CGAACCCGTT     120
160 CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCCC TGAAGGAGGA CGGGGACGTG     180

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162 GTGGTGGTGG TCTTTGACGC CAAGGCCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC      240
164 AAGGCGGGCC GGGCCCCCAC CCCGGAGGAC TTTCCCGGGC AGCTGGCCCT CATCAAGGAG      300
166 TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG      360
168 CTGGCCACCC TGGCCAAGCG GCGGAAAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC      420
170 GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC      480
172 CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCTGCG GCCCGGAGCA GTGGGTGGAC      540
174 TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG      600
176 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG      660
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180 TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGACTT CGGGAGGCGC      780
182 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGGAAGCCTC      840
184 CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT      900
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192 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC     1140
194 CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT     1200
196 GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG     1260
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200 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG     1380
202 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCTGGC CGGCCACCCC     1440
204 TTCAACCTCA ACTCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT     1500
206 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC     1560
208 CTCCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC     1620
210 AAGAACACCT ACATAGACCC CTTGCCCCGC CTGGTCCACC CCAAGACCGG CCGGCTCCAC     1680
212 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCACCTG     1740
214 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG     1800
216 GAGGGCTGGG TGCTGGTGGT CTTGGAATAC AGCCAGATTG AGCTTCGGGT CCTGGCCAC     1860
218 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTAGGAGG GGAGGGACAT CCACACCCAG     1920
220 ACCGCCAGCT GGATGTTCCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG     1980
222 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG     2040
224 CTTTCCATCC CCTACGAGGA GCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC     2100
226 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG     2160
228 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC     2220
230 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG     2280
232 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG     2340
234 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT     2400
236 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCCTGA GGTGGAGGTG     2460
238 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG                                     2496

240 (2) INFORMATION FOR SEQ ID NO: 3:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 2504 base pairs
244 (B) TYPE: nucleic acid
245 (C) STRANDEDNESS: double
246 (D) TOPOLOGY: linear
248 (ii) MOLECULE TYPE: DNA (genomic)
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
254 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC      60
256 CACCTGGCCT ACCGCACCTT CTTGCCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG      120

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258 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC 180
260 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG 240
262 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC 300
264 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC 360
266 GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC 420
268 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG 480
270 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG 540
272 GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC 600
274 GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG 660
276 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC 720
278 CTCAGGCTCT CTTGGAGCT CTCCCGGGTG CGCACCAGAC TCCCCCTGGA GGTGGACCTC 780
280 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC 840
282 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC 900
284 TGGCCCCCGC CGGAAGGGGC CTTCTGTGGC TTCGTCTCT CCCGCCCCGA GCCCATGTGG 960
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290 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC 1140
292 CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GCGCTACGG GGGGGAGTGG 1200
294 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG 1260
296 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCCTCCT 1320
298 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC 1380
300 CTTTCCCTGG AGCTTGCGGA GGAGATCCCG CGCCTCGAGG AGGAGGTCTT CCGCTTGCGC 1440
302 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT 1500
304 AGGTGTCCTG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG 1560
306 CTGGAGGCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC 1620
308 ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC 1680
310 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC 1740
312 CCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC 1800
314 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
316 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
318 CACACCCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCTGATG 1980
320 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
322 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
324 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
326 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
328 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
330 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCTT CCGGGAGATG GGGGCCCGCA 2340
332 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
334 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
336 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCAAGGG TTAG 2504

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu

## RAW SEQUENCE LISTING

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358	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
359			35					40				45		
361	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val
362		50					55				60			
364	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
365	65					70				75				80
367	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
368				85					90					95
370	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg
371				100					105				110	
373	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala
374			115					120				125		
376	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
377		130					135					140		
379	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
380	145				150					155				160
382	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
383				165					170					175
385	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser
386			180						185				190	
388	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys
389		195					200					205		
391	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp
392		210					215					220		
394	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp
395	225				230					235				240
397	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu
398				245					250				255	
400	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg
401			260					265					270	
403	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
404		275					280					285		
406	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro
407		290				295					300			
409	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp
410	305				310					315				320
412	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg
413				325					330					335
415	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly
416			340					345					350	
418	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly
419		355					360					365		
421	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro
422		370				375					380			
424	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp
425	385				390					395				400

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/941,193A

DATE: 07/23/2002  
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Input Set : A:\Seqsub2.app  
Output Set: N:\CRF3\07232002\I941193A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029  
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380  
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396  
Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290  
Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833

## VERIFICATION SUMMARY

DATE: 07/23/2002

PATENT APPLICATION: US/09/941,193A

TIME: 13:04:52

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\07232002\I941193A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48  
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96  
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176  
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192  
L:1165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208  
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224  
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240  
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256  
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L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336  
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352  
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400  
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416  
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544  
L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592  
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